AMENDMENTS TO THE CLAIMS:

Please amend claims as follows:

1 – 24. (Cancelled).

25. (Currently amended) An antagonist of a ligand for an epitope or footprint domain for binding integrins, in which said epitope comprises **a member selected from the group consisting of :**

(A) strands A and G of domain 1 of ICAM-4 (SEQ ID NO: 1), wherein said A strand (SEQ ID NO: 2) is defined by amino acid residues 17 to 27 of ICAM-4 and said G strand (SEQ ID NO: 3) is defined by amino acid residues 90 to 100 of ICAM-4, ~~**or in which said epitope is modified in that said A strand is replaced by strand F on**~~

(B) strands F and G of domain 1 of ICAM-4, wherein said F strand (SEQ ID NO: 4) is defined by amino acid residues 77 to 87 of ICAM-4, ~~**or**~~

(C) strands A and C of domain 1 of ICAM-4 and ~~**in which said epitope is**~~ further defined by amino acid residues W66 on strand E of domain 1 of ICAM-4 and K118 on strand B of domain 2 of ICAM-4, wherein said E strand ~~**(SEQ ID NO: 5)**~~ is defined by amino acid residues ~~**160 to 170**~~ **65 to 75** of ICAM-4 **(SEQ ID NO:1)** and said B strand (SEQ ID NO: 6) is defined by amino acid residues 116 to 126 of ICAM-4,

and

(D) strands F and G of domain 1 of ICAM-4 and further defined by amino acid residues W66 on strand E of domain 1 of ICAM-4 and K118 on strand B of domain 2 of ICAM-4; ~~**or an antagonist of a functional homologue of said epitope,**~~ **;** and in which said footprint domain comprises a first epitope **selected from the group of (A), (B), (C)**

and (D) ~~as defined for said epitope above~~ and a second epitope comprising strand C and strand F of domain 1 of ICAM-4 and a CE loop of domain 2 of ICAM-4, wherein said C strand (SEQ ID NO: 7) is defined by amino acid residues 47 to 54 of ICAM-4, said F strand (SEQ ID NO: 4) is defined by amino acid residues 77 to 87 of ICAM-4 and said CE loop (SEQ ID NO: 8) is defined by amino acid residues 150 to 158 of ICAM-4~~, or an antagonist of a functional homologue of said footprint domain~~.

26. (Currently amended) The antagonist of claim 25, in which said antagonist ~~has or~~ consists ~~essentially~~ of three, four, five, six, seven, eight, or nine ~~or more~~ amino acid residues of said A, C, F or G strands or said CE loop of ICAM-4~~, or a functional homologue thereof~~.

27. (Previously presented) The antagonist of claim 25, in which said antagonist defined by ICAM-4 strand A includes amino acid residues F18, W19 and V20 of ICAM-4.

28. (Currently amended) The antagonist of claim 27, in which said antagonist ~~or its active site has or~~ consists ~~essentially~~ of an amino acid sequence as defined in SEQ ID NO: 9.

29. (Canceled).

30. (Withdrawn) The antagonist of claim 25, in which said antagonist defined by ICAM-4 strand F includes amino acid residues T91, W93 and R97 of ICAM-4.

31. (Withdrawn) The antagonist of claim 30, in which said antagonist or its active site has or consists essentially of an amino acid sequence as defined in SEQ ID NO: 11.

32. (Withdrawn) The antagonist of claim 25, in which said antagonist defined by ICAM-4 strand G includes amino acid residues R92, A94, T95, S96 and R97 of ICAM-4.

33. (Withdrawn) The antagonist of claim 32, in which said antagonist or its active site has or consists essentially of an amino acid sequence as defined in SEQ ID NO: 10.

34. (Withdrawn) The antagonist of claim 25, in which said antagonist defined by ICAM-4 CE loop includes amino acid residues E151 and T154 of ICAM-4.

35. (New) An antagonist of a ligand for an epitope or footprint domain for binding integrins, wherein said antagonist is selected from the group consisting of

(I) a low molecular weight compound which binds to the epitope and/or footprint domain to reduce adhesion between the epitope and/or footprint domain and its ligands;

(II) a peptide comprising amino acid residues of the A, C, F, or G strands of the CE loop of ICAM-4; and

(III) a member selected from the group of peptides, drugs and antibodies that binds an ICAM-4 ligand so as to reduce adhesion of the ligand to the epitope and/or footprint domain;

wherein said epitope comprises a member selected from the group consisting of:

(A) strands A and G of domain 1 of ICAM-4 (SEQ ID NO: 1), wherein said A strand (SEQ ID NO: 2) is defined by amino acid residues 17 to 27 of ICAM-4 and said G strand (SEQ ID NO: 3) is defined by amino acid residues 90 to 100 of ICAM-4,

(B) strands F and G of domain 1 of ICAM-4, wherein said F strand (SEQ ID NO: 4) is defined by amino acid residues 77 to 87 of ICAM-4,

(C) strands A and G of domain 1 of ICAM-4 and further defined by amino acid residues W66 on strand E of domain 1 of ICAM-4 and K118 on strand B of domain 2 of ICAM-4, wherein said E strand is defined by amino acid residues 65 to 75 of ICAM-4 (SEQ ID NO 1) and said B strand (SEQ ID NO: 6) is defined by amino acid residues 116 to 126 of ICAM-4, and

(D) strands F and G of domain 1 of ICAM-4 and further defined by amino acid residues W66 on strand E of domain 1 of ICAM-4 and K118 on strand B of domain 2 of ICAM-4 ;

and wherein said footprint domain comprises a first epitope selected from the group listed as (A)-(D) above and a second epitope comprising strand C and strand F of domain 1 of ICAM-4 and a CE loop of domain 2 of ICAM-4, wherein said C strand (SEQ ID NO: 7) is defined by amino acid residues 47 to 54 of ICAM-4, said F strand (SEQ ID NO: 4) is defined by amino acid residues 77 to 87 of ICAM-4 and said CE loop (SEQ ID NO: 8) is defined by amino acid residues 150 to 158 of ICAM-4.

36. (new) The antagonist of claim 35, wherein said antagonist is a low molecular weight compound which binds to the epitope and/or footprint domain to reduce adhesion between the epitope and/or footprint domain and its ligands.

37. (new) The antagonist of claim 35, wherein said antagonist is a drug that binds an ICAM-4 ligand so as to reduce adhesion of the ligand to the epitope and/or footprint domain.